

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/643,755

Source: O/PE

Date Processed by STIC: 8-30-2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY
EITHER:**

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT
COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY
or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT,
WITH A NOTICE TO COMPLY**

**FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER,
703-308-4212.**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:**

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/643,755

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleic
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 Wrapped Aminos
The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 Variable Length
Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (bx) feature section that some may be missing.

7 PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

8 Skipped Sequences (OLD RULES)
Sequence(s) missing. If Intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 Skipped Sequences (NEW RULES)
Sequence(s) missing. If Intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence-Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 Use of <213>Organism (NEW RULES)
Sequence(s) are missing this mandatory field or its response.

12 Use of <220>Feature (NEW RULES)
Sequence(s) 4 are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/643,755

DATE: 08/30/2000
 TIME: 14:32:19

Input Set : A:\Sequence
 Output Set: N:\CRF3\08302000\I643755.raw

Does Not Comply
 Corrected Diskette Needed

4 <110> APPLICANT: van Rooijen, Gijs
 5 Keon, Richard Glenn
 6 Boothe, Joseph
 7 Shen, Yin
 10 <120> TITLE OF INVENTION: Commercial Production of Chymosin in Plants
 12 <130> FILE REFERENCE: 9369-153
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/643,755
 C--> 15 <141> CURRENT FILING DATE: 2000-08-23
 17 <160> NUMBER OF SEQ ID NOS: 4
 19 <170> SOFTWARE: PatentIn Ver. 2.0
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 1173
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Bovine
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (1)..(1173)
 30 <400> SEQUENCE: 1
 31 atg aac ttc ctt aag tct ttc cct tac gct ttc ctt tgt ttc ggt 48
 32 Met Asn Phe Leu Lys Ser Phe Pro Phe Tyr Ala Phe Leu Cys Phe Gly
 33 1 5 10 15
 35 caa tac ttc gtt gct act cac gct gct gag atc acc acc cgc att cct 96
 36 Gln Tyr Phe Val Ala Val Thr His Ala Ala Glu Ile Thr Arg Ile Pro
 37 20 25 30
 39 ctc tac aaa ggt aag tct ctc cgt aag gcg ctg aag gaa cat gga ctt 144
 40 Leu Tyr Lys Gly Lys Ser Leu Arg Lys Ala Leu Lys Glu His Gly Leu
 41 35 40 45
 43 cta gaa gac ttc ttg cag aaa caa cag tat ggc atc agc agc aag tac 192
 44 Leu Glu Asp Phe Leu Gln Lys Gln Gln Tyr Gly Ile Ser Ser Lys Tyr
 45 50 55 60
 47 tcc ggc ttc ggt gaa gtt gct agc gtg cca ctt acc aac tac ctt gat 240
 48 Ser Gly Phe Gly Glu Val Ala Ser Val Pro Leu Thr Asn Tyr Leu Asp
 49 65 70 75 80
 51 agt caa tac ttt ggg aag atc tac ctc gga acc ccg cct caa gag ttc 288
 52 Ser Gln Tyr Phe Gly Lys Ile Tyr Leu Gly Thr Pro Pro Gln Glu Phe
 53 85 90 95
 55 acc gtt ctc ttt gat act ggt tcc tct gac ttc tgg gtt ccc tct atc 336
 56 Thr Val Leu Phe Asp Thr Gly Ser Ser Asp Phe Trp Val Pro Ser Ile
 57 100 105 110
 59 tac tgc aag agc aat gcc tgc aag aac cac caa aga ttc gat ccg aga 384
 60 Tyr Cys Lys Ser Asn Ala Cys Lys Asn His Gln Arg Phe Asp Pro Arg
 61 115 120 125
 63 aag tcg tcc acc ttc cag aac tta ggc aaa ccc ttg tct ata cac tac 432
 64 Lys Ser Ser Thr Phe Gln Asn Leu Gly Lys Pro Leu Ser Ile His Tyr
 65 130 135 140
 67 ggt aca ggt agc atg caa gga atc tta ggc tat gat acc gtc act gtc 480
 68 Gly Thr Gly Ser Met Gln Gly Ile Leu Gly Tyr Asp Thr Val Thr Val

see p. 4, 6

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/643,755

DATE: 08/30/2000
TIME: 14:32:19

Input Set : A:\Sequence
Output Set: N:\CRF3\08302000\I643755.raw

69	145	150	155	160	
71	tcc aac att gtg gac att caa cag aca gta gga ctt agc acc caa gaa				528
72	Ser Asn Ile Val Asp Ile Gln Gln Thr Val Gly Leu Ser Thr Gln Glu				
73	165	170	175		
75	cca ggt gat gtc ttc acc tat gca gaa ttc gat ggc atc ctt ggt atg				576
76	Pro Gly Asp Val Phe Thr Tyr Ala Glu Phe Asp Gly Ile Leu Gly Met				
77	180	185	190		
79	gca tac cca tcg ctc gcg tca gag tac tcg ata cct gtg ttt gac aac				624
80	Ala Tyr Pro Ser Leu Ala Ser Glu Tyr Ser Ile Pro Val Phe Asp Asn				
81	195	200	205		
83	atg atg aac cga cac cta gta gct caa gac ttg ttc tcg gtt tac atg				672
84	Met Met Asn Arg His Leu Val Ala Gln Asp Leu Phe Ser Val Tyr Met				
85	210	215	220		
87	gac agg aat ggc cag gag agc atg ctc acg ctt gga gct att gat cca				720
88	Asp Arg Asn Gly Gln Glu Ser Met Leu Thr Leu Gly Ala Ile Asp Pro				
89	225	230	235		240
91	tcc tac tac aca gga tct ctt cac tgg gtt cca gtc act gtg cag cag				768
92	Ser Tyr Tyr Thr Gly Ser Leu His Trp Val Pro Val Thr Val Gln Gln				
93	245	250	255		
95	tac tgg caa ttc act gtg gac agt gtc acc atc agc ggt gtg gtt gtt				816
96	Tyr Trp Gln Phe Thr Val Asp Ser Val Thr Ile Ser Gly Val Val Val				
97	260	265	270		
99	gca tgt gaa ggt gga tgt caa gct atc ttg gat acc ggt acg tcc aag				864
100	Ala Cys Glu Gly Cys Gln Ala Ile Leu Asp Thr Gly Thr Ser Lys				
101	275	280	285		
103	ctg gtc gga cct agc agc gac att ctc aac att cag caa gct att gga				912
104	Leu Val Gly Pro Ser Ser Asp Ile Leu Asn Ile Gln Gln Ala Ile Gly				
105	290	295	300		
107	gcc aca cag aac cag tac ggt gag ttt gac ata gat tgc gac aac ctt				960
108	Ala Thr Gln Asn Gln Tyr Gly Glu Phe Asp Ile Asp Cys Asp Asn Leu				
109	305	310	315		320
111	agc tac atg cct aca gtt gtc ttt gag atc aac ggc aag atg tac cca				1008
112	Ser Tyr Met Pro Thr Val Val Phe Glu Ile Asn Gly Lys Met Tyr Pro				
113	325	330	335		
115	ctg acc ccc tcc gcc tat acc agc cag gat caa ggg ttc tgc acc agt				1056
116	Leu Thr Pro Ser Ala Tyr Thr Ser Gln Asp Gln Gly Phe Cys Thr Ser				
117	340	345	350		
119	gga ttc cag agt gag aac cat tcc cag aaa tgg atc ttg gga gat gtg				1104
120	Gly Phe Gln Ser Glu Asn His Ser Gln Lys Trp Ile Leu Gly Asp Val				
121	355	360	365		
123	tcc att cgt gag tac tac agc gtc ttt gac agg gcc aac aac ctc gtt				1152
124	Phe Ile Arg Glu Tyr Tyr Ser Val Phe Asp Arg Ala Asn Asn Leu Val				
125	370	375	380		
127	ggg cta gct aaa gca atc tga				1173
128	Gly Leu Ala Lys Ala Ile				
129	385	390			
132	<210> SEQ ID NO: 2				
133	<211> LENGTH: 390				
134	<212> TYPE: PRT				

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/643,755

DATE: 08/30/2000

TIME: 14:32:19

Input Set : A:\Sequence
Output Set: N:\CRF3\08302000\I643755.raw

135 <213> ORGANISM: Bovine
137 <400> SEQUENCE: 2
138 Met Asn Phe Leu Lys Ser Phe Pro Phe Tyr Ala Phe Leu Cys Phe Gly
139 1 5 10 15
141 Gln Tyr Phe Val Ala Val Thr His Ala Ala Glu Ile Thr Arg Ile Pro
142 20 25 30
144 Leu Tyr Lys Gly Lys Ser Leu Arg Lys Ala Leu Lys Glu His Gly Leu
145 35 40 45
147 Leu Glu Asp Phe Leu Gln Lys Gln Tyr Gly Ile Ser Ser Lys Tyr
148 50 55 60
150 Ser Gly Phe Gly Glu Val Ala Ser Val Pro Leu Thr Asn Tyr Leu Asp
151 65 70 75 80
153 Ser Gln Tyr Phe Gly Lys Ile Tyr Leu Gly Thr Pro Pro Gln Glu Phe
154 85 90 95
156 Thr Val Leu Phe Asp Thr Gly Ser Ser Asp Phe Trp Val Pro Ser Ile
157 100 105 110
159 Tyr Cys Lys Ser Asn Ala Cys Lys Asn His Gln Arg Phe Asp Pro Arg
160 115 120 125
162 Lys Ser Ser Thr Phe Gln Asn Leu Gly Lys Pro Leu Ser Ile His Tyr
163 130 135 140
165 Gly Thr Gly Ser Met Gln Gly Ile Leu Gly Tyr Asp Thr Val Thr Val
166 145 150 155 160
168 Ser Asn Ile Val Asp Ile Gln Gln Thr Val Gly Leu Ser Thr Gln Glu
169 165 170 175
171 Pro Gly Asp Val Phe Thr Tyr Ala Glu Phe Asp Gly Ile Leu Gly Met
172 180 185 190
174 Ala Tyr Pro Ser Leu Ala Ser Glu Tyr Ser Ile Pro Val Phe Asp Asn
175 195 200 205
177 Met Met Asn Arg His Leu Val Ala Gln Asp Leu Phe Ser Val Tyr Met
178 210 215 220
180 Asp Arg Asn Gly Gln Glu Ser Met Leu Thr Leu Gly Ala Ile Asp Pro
181 225 230 235 240
183 Ser Tyr Tyr Thr Gly Ser Leu His Trp Val Pro Val Thr Val Gln Gln
184 245 250 255
186 Tyr Trp Gln Phe Thr Val Asp Ser Val Thr Ile Ser Gly Val Val Val
187 260 265 270
189 Ala Cys Glu Gly Gly Cys Gln Ala Ile Leu Asp Thr Gly Thr Ser Lys
190 275 280 285
192 Leu Val Gly Pro Ser Ser Asp Ile Leu Asn Ile Gln Gln Ala Ile Gly
193 290 295 300
195 Ala Thr Gln Asn Gln Tyr Gly Glu Phe Asp Ile Asp Cys Asp Asn Leu
196 305 310 315 320
198 Ser Tyr Met Pro Thr Val Val Phe Glu Ile Asn Gly Lys Met Tyr Pro
199 325 330 335
201 Leu Thr Pro Ser Ala Tyr Thr Ser Gln Asp Gln Gly Phe Cys Thr Ser
202 340 345 350
204 Gly Phe Gln Ser Glu Asn His Ser Gln Lys Trp Ile Leu Gly Asp Val
205 355 360 365
207 Phe Ile Arg Glu Tyr Tyr Ser Val Phe Asp Arg Ala Asn Asn Leu Val

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/643,755

DATE: 08/30/2000
TIME: 14:32:19

Input Set : A:\Sequence
Output Set: N:\CRF3\08302000\I643755.raw

208	370	375	380
210	Gly Leu Ala Lys Ala Ile		
211	385	390	
214	<210> SEQ ID NO: 3		
215	<211> LENGTH: 3957		
216	<212> TYPE: DNA		
217	<213> ORGANISM: Artificial Sequence		
219	<220> FEATURE:		
220	<221> NAME/KEY: CDS		
221	<222> LOCATION: (1554)..(2726)		
223	<220> FEATURE:		
224	<223> OTHER INFORMATION: Description of Artificial Sequence (Figure 2)		
226	SEQUENCE: 3		
227	ctgcaggaaat tcattgtact cccagttatca ttatagtgaa agttttggct ctctcgccgg 60		
229	tggttttta cctctattta aaggggtttt ccacctaataaattctgtat catttcact 120		
231	ttacttgtta cttaatttc tcataatctt tgggtaaat tatacgtttt cccacacacgaa 180		
233	tatccctaca aattttat tggtaaaca ttttcaaaacc gcataaaattt ttatgaagtc 240		
235	ccgtctatct ttaatgtatg ctaacatttt catattgaaa tatataaattt acttaatttt 300		
237	agcgttggta gaaagcataa agatttatc ttattcttct tcatataaat gtttaataat 360		
239	caataataaac aaattcttta cttaaagaag gatttccat ttttataattt aaaaatataat 420		
241	ttatcaaataa ttttcaacc acgtaaaatc cataataataa agttgttca aaagtaataaa 480		
243	aatttaactc cataattttt ttattcact gatcttaaaag caacaccagg tgacacaact 540		
245	agccattttt ttctttaat aaaaaatcc aatttacatt gtatttttt tatacaatga 600		
247	aatttcacc aacaatcat ttgtggatt tctgaagcaa gtcatgttat gcaaaattt 660		
249	ataattccca ttgacacta cggaaatgaaatc tgaatgtcg cttttacatg cgagacacat 720		
251	cttcattaaat aattttataa atagttacta tattcaatata ttcatatatac aaataactcaa 780		
253	tattacttct aaaaaattaa ttagatataa tttaataattt acttttttaa tttaatgttt 840		
255	aattgtgaa ttgtgacta ttgattttt attctactat gtttaatgg ttttataatg 900		
257	agtttaaagt aaataataatg aatgttagtag agtgttagag tggatccata aaccataaaac 960		
259	tataacattt atggtgact aattttcataa tttttcttata ttcttttacc tttttttgg 1020		
261	atgtaaatggcc gtaacttagaa ttacagtggg tgccatggc actctgtggc cttttggcc 1080		
263	atgcattgggt ctgcgcag aaaaagacaa agaacaaga aaaaagacaa aacagagaga 1140		
265	caaaacgcac tcaacacaacc aactcaaattt agtcaactggc tgatcaatg cgcgcgtcc 1200		
267	atgtatgtct aatgcctatg caagcaaca cgtgccttac atgcacttta aatggctcac 1260		
269	ccatctcaac ccacacacaa acacattggc ttcttcttca tcattaccac aaccacctgt 1320		
271	atatttcatt tctttccgc caccatattt tcttcacttca aacacacgtc aaccgtcata 1380		
273	tgctgtcat cccatgcacca aatccatgtt catgttccaa ccaccttctc ttcttataaa 1440		
275	tacccataaa tacctctaat atcacttact ttcttcataa tccatccatc cagactacta 1500		
277	ctactctact actataatac cccaaacccaa ctcatattca atactactt act atg 1556		
278		Met	
279		1	
281	aac ttc ctt aag tct ttc cct ttc tac gct ttc ctt tgt ttc ggt caa	1604	
282	Asn Phe Leu Lys Ser Phe Pro Phe Tyr Ala Phe Leu Cys Phe Gly Gln		
283	5 10 15		
285	tac ttc gtt gtt act cac gct gct gag atc acc cgc att cct ctc	1652	
286	Tyr Phe Val Ala Val Thr His Ala Ala Glu Ile Thr Arg Ile Pro Leu		
287	20 25 30		
289	tac aaa ggt aag tct ctc cgt aag gcg ctg aag gaa cat gga ctt cta	1700	
290	Tyr Lys Gly Ser Leu Arg Lys Ala Leu Lys Glu His Gly Leu		

More specific
source of genetic
material in the
artificial sequence

See #12 on
Error Summary
Sheet.

RAW SEQUENCE LISTING DATE: 08/30/2000
PATENT APPLICATION: US/09/643,755 TIME: 14:32:19

Input Set : A:\Sequence
Output Set: N:\CRF3\08302000\1643755.raw

291	35	40	45	1748
293	gaa gac ttc ttg cag aaa caa cag tat ggc atc agc agc aag tac tcc			
294	Glu Asp Phe Leu Gln Lys Gln Gln Tyr Gly Ile Ser Ser Lys Tyr Ser			
295	50	55	60	65
297	ggc ttc ggt gaa gtt gct agc gtg cca ctt acc aac tac ctt gat agt			
298	Gly Phe Gly Glu Val Ala Ser Val Pro Leu Thr Asn Tyr Leu Asp Ser			
299	70	75	80	
301	caa tac ttt ggg aag atc tac ctc gga acc ccc cct caa gag ttc acc			1844
302	Gln Tyr Phe Gly Lys Ile Tyr Leu Gly Thr Pro Pro Gln Glu Phe Thr			
303	85	90	95	
305	gtt ctc ttt gat act ggt tcc tct gac ttc tgg gtt ccc tct atc tac			
306	Val Leu Phe Asp Thr Gly Ser Ser Asp Phe Trp Val Pro Ser Ile Tyr			
307	100	105	110	
309	tgc aag agc aat gcc tgc aag aac cac caa aga ttc gat ccg aga aag			1940
310	Cys Lys Ser Asn Ala Cys Lys Asn His Gln Arg Phe Asp Pro Arg Lys			
311	115	120	125	
313	tcg tcc acc ttc cag aac tta ggc aaa ccc ttg tct ata cac tac ggt			
314	Ser Ser Thr Phe Gln Asn Leu Gly Lys Pro Leu Ser Ile His Tyr Gly			
315	130	135	140	145
317	aca ggt agc atg caa gga atc tta ggc tat gat acc gtc act gtc tcc			2036
318	Thr Gly Ser Met Gln Gly Ile Leu Gly Tyr Asp Thr Val Thr Val Ser			
319	150	155	160	
321	aac att gtg gac att caa cag aca gta gga ctt agc acc caa gaa cca			2084
322	Asn Ile Val Asp Ile Gln Gln Thr Val Gly Leu Ser Thr Gln Glu Pro			
323	165	170	175	
325	ggt gat gtc ttc acc tat gca gaa ttc gat ggc atc ctt ggt atg gca			2132
326	Gly Asp Val Phe Thr Tyr Ala Glu Phe Asp Gly Ile Leu Gly Met Ala			
327	180	185	190	
329	tac cca tcg ctc gcg tca gag tac tcg ata cct gtc ttt gac aac atg			2180
330	Tyr Pro Ser Leu Ala Ser Glu Tyr Ser Ile Pro Val Phe Asp Asn Met			
331	195	200	205	
333	atg aac cga cac cta gta gct caa gac ttg ttc tcg gtt tac atg gac			2228
334	Met Asn Arg His Leu Val Ala Gln Asp Leu Phe Ser Val Tyr Met Asp			
335	210	215	220	225
337	agg aat ggc cag gag agc atg ctc acg ctt gga gct att gat cca tcc			2276
338	Arg Asn Gly Gln Glu Ser Met Leu Thr Leu Gly Ala Ile Asp Pro Ser			
339	230	235	240	
341	tac tac aca gga tct ctt cac tgg gtt cca gtc act gtc cag cag tac			2324
342	Tyr Tyr Thr Gly Ser Leu His Trp Val Pro Val Thr Val Gln Gln Tyr			
343	245	250	255	
345	tgg caa ttc act gtg gac agt gtc acc atc agc ggt gtc gtt gtt gca			
346	Trp Gln Phe Thr Val Asp Ser Val Thr Ile Ser Gly Val Val Val Ala			
347	260	265	270	
349	tgt gaa ggt gga tgt caa gct atc ttg gat acc ggt acg tcc aag ctg			2420
350	Cys Glu Gly Gly Cys Gln Ala Ile Leu Asp Thr Gly Thr Ser Lys Leu			
351	275	280	285	
353	gtc gga cct agc agc gac att ctc aac att cag caa gct att gga gcc			
354	Val Gly Pro Ser Ser Asp Ile Leu Asn Ile Gln Gln Ala Ile Gly Ala			
355	290	295	300	305

09/69 755

Missing mandatory <220> and
<223> features to explain
artificial sequence. See # 12
on Error Summary Sheet.

<210> 4

<211> 390

<212> PRT

<213> Artificial Sequence

<400> 4

Met Asn Phe Leu Lys Ser Phe Pro Phe Tyr Ala Phe Leu Cys Phe Gly

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/643,755

DATE: 08/30/2000

TIME: 14:32:20

Input Set : A:\Sequence

Output Set: N:\CRF3\08302000\I643755.raw

L:14 M:270 C: Current Application Number differs, Replaced Application Number

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:429 M:258 W: Mandatory Feature missing, <220> FEATURE:

L:429 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):

1. This application clearly fails to comply with the requirements of 37 CFR 1.821 - 1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).

3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).

4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached marked-up copy of the "Raw Sequence Listing."

5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).

6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).

7. Other: _____

Applicant must provide:

An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"

An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification

A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact:

For Rules Interpretation, call (703) 308-1123
For CRF submission help, call (703) 308-4212
For PatentIn software help, call (703) 308-6856

Please return a copy of this notice with your response.